

OIKE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/265,540E

DATE: 07/31/2001

TIME: 15:02:54

Input Set : A:\DX0804K.txt

Output Set: N:\CRF3\07312001\I265540E.raw

ENTERED

3 <110> APPLICANT: Parham, Christi L.  
 4 Moore, Kevin W.  
 5 Murgolo, Nicholas J.  
 6 Bazan, J. Fernando  
 8 <120> TITLE OF INVENTION: HUMAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS  
 10 <130> FILE REFERENCE: DX0804K  
 12 <140> CURRENT APPLICATION NUMBER: 09/265,540E  
 13 <141> CURRENT FILING DATE: 1999-03-08  
 15 <150> PRIOR APPLICATION NUMBER: 60/077,329  
 16 <151> PRIOR FILING DATE: 1999-03-09  
 18 <160> NUMBER OF SEQ ID NOS: 6  
 20 <170> SOFTWARE: PatentIn version 3.1  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 1381  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Homo sapiens  
 27 <220> FEATURE:  
 28 <221> NAME/KEY: CDS  
 29 <222> LOCATION: (132)..(1064)  
 30 <223> OTHER INFORMATION:  
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 34 <221> NAME/KEY: misc\_feature  
 35 <222> LOCATION: (567)..(567)  
 36 <223> OTHER INFORMATION: unknown nucleotide  
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 40 <221> NAME/KEY: misc\_feature  
 41 <222> LOCATION: (573)..(573)  
 42 <223> OTHER INFORMATION: unknown nucleotide  
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 46 <221> NAME/KEY: misc\_feature  
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 48 <223> OTHER INFORMATION: unknown nucleotide  
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 52 <221> NAME/KEY: misc\_feature  
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 54 <223> OTHER INFORMATION: unknown nucleotide  
 57 <220> FEATURE:  
 58 <221> NAME/KEY: misc\_feature  
 59 <222> LOCATION: (1369)..(1369)  
 60 <223> OTHER INFORMATION: unknown nucleotide  
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 66 agatggctga gatggacaga atgctttatt ttggaaagaa acaatgttct aggtcaact 120  
 68 gagtctacca a atg cag act ttc aca atg gtt cta gaa gaa atc tgg aca 170  
 69 Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr  
 70 1 5 10  
 72 agt ctt ttc atg tgg ttt ttc tac gca ttg att cca tgt ttg ctc aca 218

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73 Ser Leu Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr  
 74 15 20 25  
 76 gat gaa gtg gcc att ctg cct gcc cct cag aac ctc tct gta ctc tca 266  
 77 Asp Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser  
 78 30 35 40 45  
 80 acc aac atg aag cat ctc ttg atg tgg agc cca gtg atc gcg cct gga 314  
 81 Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly  
 82 50 55 60  
 84 gaa aca gtg tac tat tct gtc gaa tac cag ggg gag tac gag agc ctg 362  
 85 Glu Thr Val Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu  
 86 65 70 75  
 88 tac acg agc cac atc tgg atc ccc agc agc tgg tgc tca ctc act gaa 410  
 89 Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu  
 90 80 85 90  
 92 ggt cct gag tgt gat gtc act gat gac atc acg gcc act gtg cca tac 458  
 93 Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr  
 94 95 100 105  
 96 aac ctt cgt gtc agg gcc aca ttg ggc tca cag acc tca gcc tgg agc 506  
 97 Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser  
 98 110 115 120 125  
 100 atc ctg aag cat ccc ttt aat aga aac tca acc atc ctt acc cga cct 554  
 101 Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro  
 102 130 135 140  
 104 ggg atg gag atc ncc aaa nat ggc ttc cac ctg gtt att gag ctg gag 602  
 105 Gly Met Glu Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu  
 106 145 150 155  
 108 gac ctg ggg ccc cag ttt gag ttc ctt gtg gcc tac tgg asg agg gag 650  
 109 Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu  
 110 160 165 170  
 112 cct ggt gcc gag gaa cat gtc aaa atg gtg agg agt ggg ggt att cca 698  
 113 Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro  
 114 175 180 185  
 116 gtg cac cta gaa acc atg gag cca ggg gct gca tac tgt gtg aag gcc 746  
 117 Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala  
 118 190 195 200 205  
 120 cag aca ttc gtg aag gcc att ggg arg tac agc gcc ttc agc cag aca 794  
 121 Gln Thr Phe Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr  
 122 210 215 220  
 124 gaa tgt gtg gar gtg caa gga gag gcc att ccc ctg gta ctg gcc ctg 842  
 125 Glu Cys Val Glu Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu  
 126 225 230 235  
 128 ttt gcc ttt gtt ggc ttc atg ctg atc ctt gtg gtc gtg cca ctg ttc 890  
 129 Phe Ala Phe Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe  
 130 240 245 250  
 132 gtc tgg aaa atg ggc cgg ctg ctc cag tac tcc tgt tgc ccc gtg gtg 938  
 133 Val Trp Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val  
 134 255 260 265  
 136 gtc ctc cca gac acc ttg aaa ata acc aat tca ccc cag aag tta atc 986  
 137 Val Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile

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1 38 270          275          280          285
1 40 agc tgc aga agg gag gag gtg gat gcc tgt gcc acg gct gtg atg tct      1034
1 41 Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser
1 42          290          295          300
1 44 cct gag gaa ctc ctc agg gcc tgg atc tca taggtttgcg gaagggccca      1084
1 45 Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser
1 46          305          310
1 48 ggtgaagccg agaacctggt ctgcatgaca tggaaaccat gaggggacaa gttgtgtttc      1144
1 50 tgttttccgc cacggacaag ggatgagaga agtaggaaga gcctgttgct tacaagtcta      1204
1 52 gaagcaacca tcagaggcag ggtggtttgt ckaacagaac aaytgactga ggytakrggg      1264
1 54 gwtgtgacct ctagactktg ggstkscayt tgcwtggytg agcaaccctg ggaaaagtga      1324
1 56 cttcatccct tnggtccnaa gttttctcat ctgtaatggg ggatncctac aaaactg      1381

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159 &lt;210&gt; SEQ ID NO: 2

160 &lt;211&gt; LENGTH: 311

161 &lt;212&gt; TYPE: PRT

162 &lt;213&gt; ORGANISM: Homo sapiens

164 &lt;220&gt; FEATURE:

165 &lt;221&gt; NAME/KEY: misc\_feature

166 &lt;222&gt; LOCATION: (146)..(146)

167 &lt;223&gt; OTHER INFORMATION: The 'Xaa' at location 146 stands for Thr, Ala, Pro, or Ser.

169 &lt;220&gt; FEATURE:

170 &lt;221&gt; NAME/KEY: misc\_feature

171 &lt;222&gt; LOCATION: (148)..(148)

172 &lt;223&gt; OTHER INFORMATION: The 'Xaa' at location 148 stands for Asn, Asp, His, or Tyr.

174 &lt;220&gt; FEATURE:

175 &lt;221&gt; NAME/KEY: misc\_feature

176 &lt;222&gt; LOCATION: (171)..(171)

177 &lt;223&gt; OTHER INFORMATION: The 'Xaa' at location 171 stands for Arg, or Thr.

179 &lt;220&gt; FEATURE:

180 &lt;221&gt; NAME/KEY: misc\_feature

181 &lt;222&gt; LOCATION: (214)..(214)

182 &lt;223&gt; OTHER INFORMATION: The 'Xaa' at location 214 stands for Arg, or Lys.

184 &lt;220&gt; FEATURE:

185 &lt;221&gt; NAME/KEY: misc\_feature

186 &lt;222&gt; LOCATION: (567)..(567)

187 &lt;223&gt; OTHER INFORMATION: unknown nucleotide

189 &lt;220&gt; FEATURE:

190 &lt;221&gt; NAME/KEY: misc\_feature

191 &lt;222&gt; LOCATION: (573)..(573)

192 &lt;223&gt; OTHER INFORMATION: unknown nucleotide

194 &lt;220&gt; FEATURE:

195 &lt;221&gt; NAME/KEY: misc\_feature

196 &lt;222&gt; LOCATION: (1336)..(1336)

197 &lt;223&gt; OTHER INFORMATION: unknown nucleotide

199 &lt;220&gt; FEATURE:

200 &lt;221&gt; NAME/KEY: misc\_feature

201 &lt;222&gt; LOCATION: (1342)..(1342)

202 &lt;223&gt; OTHER INFORMATION: unknown nucleotide

204 &lt;220&gt; FEATURE:

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2 05 <221> NAME/KEY: misc\_feature  
 2 06 <222> LOCATION: (1369)..(1369)  
 2 07 <223> OTHER INFORMATION: unknown nucleotide  
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 2 12 1 5 10 15  
 2 15 Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp Glu Val  
 2 16 20 25 30  
 2 19 Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser Thr Asn Met  
 2 20 35 40 45  
 2 23 Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly Glu Thr Val  
 2 24 50 55 60  
 2 27 Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu Tyr Thr Ser  
 2 28 65 70 75 80  
 2 31 His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu Gly Pro Glu  
 2 32 85 90 95  
 2 35 Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr Asn Leu Arg  
 2 36 100 105 110  
 2 39 Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser Ile Leu Lys  
 2 40 115 120 125  
 2 43 His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro Gly Met Glu  
 2 44 130 135 140  
 W-→ 2 47 Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu Asp Leu Gly  
 2 48 145 150 155 160  
 W-→ 2 51 Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu Pro Gly Ala  
 2 52 165 170 175  
 2 55 Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu  
 2 56 180 185 190  
 2 59 Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe  
 2 60 195 200 205  
 2 63 Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val  
 2 64 210 215 220  
 2 67 Glu Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe  
 2 68 225 230 235 240  
 2 71 Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp Lys  
 2 72 245 250 255  
 2 75 Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val Leu Pro  
 2 76 260 265 270  
 2 79 Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile Ser Cys Arg  
 2 80 275 280 285  
 2 83 Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser Pro Glu Glu  
 2 84 290 295 300  
 2 87 Leu Leu Arg Ala Trp Ile Ser  
 2 88 305 310  
 2 91 <210> SEQ ID NO: 3  
 2 92 <211> LENGTH: 1244  
 2 93 <212> TYPE: DNA  
 2 94 <213> ORGANISM: Homo sapiens  
 2 96 <220> FEATURE:

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Input Set : A:\DX0804K.txt

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299 <223> OTHER INFORMATION:
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304   Arg Val Asp Pro Arg Val Arg Leu Val Ser Pro Trp Leu Thr Val Pro
305     1           5           10           15
307 tgg ttc ctg tcc tgt tgg aat gtt acc att ggg cct cct gag agc atc      97
308 Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser Ile
309           20           25           30
311 tgg gtg acg ccg gga gaa gcc tcc ctc atc atc agg ttc tcc tct ccc     145
312 Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro
313           35           40           45
315 ttc gac gtc cct ccc aac ctg ggc tat ttc cag tac tat gtc cat tay     193
316 Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Tyr
317           50           55           60
319 tgg gaa aag gcg gga atc caa aag gtt aaa ggt cct ttc aag agc aac     241
320 Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn
321 65           70           75           80
323 tcc atc gtg ttg gat ggc ttg aga ccc tta aga gaa tac tgt tta caa     289
324 Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln
325           85           90           95
327 gtg aag gcg cat ctc ttt cgc aca tcc tgc aac acc tct agg ccc ggc     337
328 Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly
329           100          105          110
331 cgc tta agc aac ata act tgc tac gaa aca atg atg gat gcc act acg     385
332 Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr
333           115          120          125
335 aag ctt caa caa gtc atc ctc atc gcc gtg gga gtc ttt ctg tcg ctg     433
336 Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu
337           130          135          140
339 gcg gcg ctg gcg ggg ggc tgt ttc ttc ctg gtg ctg aga tac aaa ggc     481
340 Ala Ala Leu Ala Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly
341 145          150          155          160
343 ctg gtg aaa tac tgg ttt cac tct ccg cca agc atc cca tca caa atc     529
344 Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile
345           165          170          175
347 gaa gag tat ctg aag gac ccg agc cag cct atc cta gag gcc ctg gac     577
348 Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu Asp
349           180          185          190
351 aag gac acg tca cca aca gat gat gcc tgg gac ttg gtg tct gtt gtt     625
352 Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val Val
353           195          200          205
355 gca ttt cca gca aag gag caa gaa gat gtt ccc caa agc act ttg acc     673
356 Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu Thr
357           210          215          220
359 caa aac tct ggt gcg gtc tgc tagcctgtgg ggtaagggct ctgagccgag     724
360 Gln Asn Ser Gly Ala Val Cys
361 225          230

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## VERIFICATION SUMMARY

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Input Set : A:\DX0804K.txt

Output Set: N:\CRF3\07312001\I265540E.raw

L:104 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:121 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:156 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:247 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:251 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:263 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2